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May 1, 2003

Ms. Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

Re: US Patent Application No. 09/870,353
For: IMPROVED NUCLEIC ACID MODIFYING ENZYMES
Inventors: Yan Wang, et al.
Filed: May 30, 2001
Our File No.: 020130-000111US

Dear Ms. Steele:

The enclosed replacement sequence listing diskette with paper copy and statement letter is being sent to you pursuant to our telephone conversation today. Please let me know if you need anything else. Thank you for your assistance.

Very truly yours,

Jean M. Lockyer, Ph.D.
Patent Agent

JML/mcd
Enclosure

SF 1456680 v1

I hereby certify that this is being send via "FedEx"on **May 1, 2003**
to:
Ms Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

TOWNSEND and TOWNSEND and CREW LLP
By: Malinda Wright

PATENT
Attorney Docket No.: 020130-000111US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

WANG *et al.*

Application No.: 09/870,353

Filed: May 30, 2001

For: IMPROVED NUCLEIC ACID MODIFYING ENZYMES

Examiner: Not yet assigned

Art Unit: 1633

SUBMISSION OF REPLACEMENT COPY OF SEQUENCE LISTING

Ms Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

Sir:

In response to the May 1, 2003 telephone request for a replacement copy of the computer readable form (CRF) of the Sequence Listing that was previously filed on August 5, 2002, Applicants submit herewith the requested replacement CFR and paper copy of the Sequence Listing.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

If it is believed that a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Jean M. Lockyer
Reg. No. 44,879

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Tel: 415-576-0200
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JML:dmw
SF 1456614 v1

#12

SEQUENCE LISTING

<110> Wang, Yan
Xi, Lei
Prosen, Dennis E.
MJ Bioworks, Inc.

<120> Improved Nucleic Acid Modifying Enzymes

<130> 020130-000111US

<140> US 09/870,353
<141> 2001-05-30

<150> US 60/207,567
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        35                  40                  45
Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
    50                  55                  60
Glu Lys Gln Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala Leu Glu
65                  70                  75                  80
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu
                85                  90                  95
Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala Ala
            100                 105                 110
Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg
        115                 120                 125
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225                 230                 235                 240
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Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
            260                 265                 270
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    290                 295                 300
Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr
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Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
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Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala
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Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
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Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu Ala
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Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met
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Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile
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Ssod7d/full-length Taq

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        35                  40                  45
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Glu Lys Gln Lys Lys Gly Gly Gly Val Thr Ser Gly Met Leu Pro Leu
65                  70                  75                  80
Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly His His Leu Ala
                85                  90                  95
Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr Ser Arg Gly Glu
            100                 105                 110
Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu Leu Lys Ala Leu
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Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp Ala Lys Ala Pro
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                245                 250                 255
Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly Val Lys Gly Ile
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Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser Leu Glu
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Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg Glu Lys
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Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp Asp Leu Ala Lys
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    690                 695                 700
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705                 710                 715                 720
Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
                725                 730                 735
Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
            740                 745                 750
Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg
        755                 760                 765
Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
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785                 790                 795                 800
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<223> Pfu-Ssod7d

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gcctacgaaa gaaacgaagt agctccaaac aagccaagtg aagaggagta tcaaagaagg 1140
ctcagggaga gctacacagg tggattcgtt aaagagccag aaaaggggtt gtgggaaaac 1200
atagtatacc tagattttag agccctatat ccctcgatta taattaccca caatgtttct 1260
cccgatactc taaatcttga gggatgcaag aactatgata tcgctcctca agtaggccac 1320
aagttctgca aggacatccc tggttttata ccaagtctct tgggacattt gttagaggaa 1380
agacaaaaga ttaagacaaa aatgaaggaa actcaagatc ctatagaaaa aatactcctt 1440
gactatagac aaaaagcgat aaaactctta gcaaattctt tctacggata ttatggctat 1500
gcaaaagcaa gatggtactg taaggagtgt gctgagagcg ttactgcctg gggaagaaag 1560
tacatcgagt tagtatggaa ggagctcgaa gaaaagtttg gatttaaagt cctctacatt 1620
gacactgatg gtctctatgc aactatccca ggaggagaaa gtgaggaaat aaagaaaaag 1680
gctctagaat ttgtaaaata cataaattca aagctccctg gactgctaga gcttgaatat 1740
gaagggtttt ataagagggg attcttcgtt acgaagaaga ggtatgcagt aatagatgaa 1800
gaaggaaaag tcattactcg tggtttagag atagttagga gagattggag tgaaattgca 1860
aaagaaactc aagctagagt tttggagaca atactaaaac acggagatgt tgaagaagct 1920
gtgagaatag taaaagaagt aatacaaaag cttgccaatt atgaaattcc accagagaag 1980
ctcgcaatat atgagcagat aacaagacca ttacatgagt ataaggcgat aggtcctcac 2040
gtagctgttg caaagaaact agctgctaaa ggagttaaaa taaagccagg aatggtaatt 2100
ggatacatag tacttagagg cgatggtcca attagcaata gggcaattct agctgaggaa 2160
tacgatccca aaaagcacaa gtatgacgca gaatattaca ttgagaacca ggttcttcca 2220
gcggtactta ggatattgga gggatttgga tacagaaagg aagacctcag ataccaaaag 2280
acaagacaag tcggcctaac ttcctggctt aacattaaaa aatccggtac cggcggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtggcaag 2460
accggccgtg gtgcggtaag cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga                                                  2535
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<210> 8
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
Pfu-Ssod7d

<400> 8

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1               5                  10                  15
Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
            20                  25                  30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
        35                  40                  45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50                  55                  60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65                  70                  75                  80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
                85                  90                  95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100                 105                 110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115                 120                 125
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Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130                 135                 140
Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
                165                 170                 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180                 185                 190
Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
        195                 200                 205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210                 215                 220
Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                 240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
                245                 250                 255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
            260                 265                 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275                 280                 285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
    290                 295                 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305                 310                 315                 320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
                325                 330                 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340                 345                 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
        355                 360                 365
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
    370                 375                 380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385                 390                 395                 400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
                405                 410                 415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
            420                 425                 430
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
        435                 440                 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450                 455                 460
Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465                 470                 475                 480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
                485                 490                 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500                 505                 510
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
        515                 520                 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530                 535                 540
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545                 550                 555                 560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565                 570                 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580                 585                 590
Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
        595                 600                 605
```

```
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610                 615                 620
Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625                 630                 635                 640
Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
                645                 650                 655
Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660                 665                 670
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675                 680                 685
Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690                 695                 700
Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705                 710                 715                 720
Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725                 730                 735
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740                 745                 750
Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
        755                 760                 765
Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770                 775                 780
Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785                 790                 795                 800
Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                805                 810                 815
Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820                 825                 830
Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
        835                 840
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<210> 9
<211> 1904
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
Sac7d-deltaTaq

<220>
<221> CDS
<222> (1)..(1904)
<223> Sac7d-deltaTaq

<400> 9
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gacacttcaa agataaagaa ggtttggaga gtaggcaaaa tggtgtcctt tacctatgac 120
gacaatggta agacaggtag aggagctgta agcgagaaag atgctccaaa agaattatta 180
gacatgttag caagagcaga aagagagaag aaaggcggcg gtgtcactag tcccaaggcc 240
ctggaggagg ccccctggcc cccgccggaa ggggccttcg tgggctttgt gctttcccgc 300
aaggagccca tgtgggccga tcttctggcc ctggccgccg ccaggggggg ccgggtccac 360
cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 420
aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgcccgg cgacgacccc 480
atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgaggggct ggcccggcgc 540
tacggcgggg agtggacgga ggaggcgggg gagcgggccg ccctttccga gaggctcttc 600
gccaacctgt gggggaggct tgagggggag gagaggctcc tttggcttta ccgggaggtg 660
gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg 720
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccggg 780
tcttccgcct ggccggccac cccttcaacc tcaactcccg ggaccagctg gaaagggtcc 840

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tctttgacga gctagggctt cccgccatcg gcaagacgga gaagaccggc aagcgctcca 900
ccagcgccgc cgtcctggag gccctccgcg aggcccaccc catcgtggag aagatcctgc 960
agtaccggga gctcaccaag ctgaagagca cctacattga ccccttgccg gacctcatcc 1020
accccaggac gggccgcctc cacacccgct tcaaccagac ggccacggcc acgggcaggc 1080
taagtagctc cgatcccaac ctccagaaca tccccgtccg caccccgctt gggcagagga 1140
tccgccgggc cttcatcgcc gaggaggggt ggctattggt ggccctggac tatagccaga 1200
tagagctcag ggtgctggcc cacctctccg gcgacgagaa cctgatccgg gtcttccagg 1260
aggggcggga catccacacg gagaccgcca gctggatgtt cggcgtcccc cgggaggccg 1320
tggacccccc gatgcgccgg gcggccaaga ccatcaactt cggggtcctc tacggcatgt 1380
cggcccaccg cctctcccag gagctagcca tcccttacga ggaggcccag gccttcattg 1440
agcgctactt tcagagcttc cccaaggtgc gggcctggat tgagaagacc ctggaggagg 1500
gcaggaggcg ggggtacgtg gagaccctct tcggccgccg ccgctacgtg ccagacctag 1560
aggcccgggt gaagagcgtg cgggaggcgg ccgagcgcat ggccttcaac atgcccgtcc 1620
agggcaccgc cgccgacctc atgaagctgg ctatggtgaa gctcttcccc aggctggagg 1680
aaatgggggc caggatgctc cttcaggtcc acgacgagct ggtcctcgag gccccaaaag 1740
agagggcgga ggccgtggcc cggctggcca aggaggtcat ggaggggtg tatcccctgg 1800
ccgtgccccc ggaggtggag gtggggatag gggaggactg gctctccgcc aaggagggca 1860
ttgatggccg cggcggaggc gggcatcatc atcatcatca ttaa                   1904
```

<210> 10
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
Sac7d-deltaTaq

<400> 10

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Met Ile Thr Asn Ser Thr Val Lys Val Lys Phe Lys Tyr Lys Gly Glu
  1               5                  10                  15
Glu Lys Glu Val Asp Thr Ser Lys Ile Lys Lys Val Trp Arg Val Gly
             20                  25                  30
Lys Met Val Ser Phe Thr Tyr Asp Asp Asn Gly Lys Thr Gly Arg Gly
         35                  40                  45
Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Asp Met Leu Ala
     50                  55                  60
Arg Ala Glu Arg Glu Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala
 65                  70                  75                  80
Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
                 85                  90                  95
Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala
            100                 105                 110
Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
        115                 120                 125
Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
    130                 135                 140
Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
145                 150                 155                 160
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
                165                 170                 175
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
            180                 185                 190
Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
        195                 200                 205
Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
    210                 215                 220
Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
225                 230                 235                 240
```

```
Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
                245                 250                 255
Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
            260                 265                 270
Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
        275                 280                 285
Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
    290                 295                 300
Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
305                 310                 315                 320
Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
                325                 330                 335
Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
            340                 345                 350
Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
        355                 360                 365
Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
    370                 375                 380
Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
385                 390                 395                 400
Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
                405                 410                 415
Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
            420                 425                 430
Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
        435                 440                 445
Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
    450                 455                 460
Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
465                 470                 475                 480
Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
                485                 490                 495
Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
            500                 505                 510
Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
        515                 520                 525
Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
    530                 535                 540
Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
545                 550                 555                 560
Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu
                565                 570                 575
Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
            580                 585                 590
Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
        595                 600                 605
Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly Ile Asp Gly Arg
    610                 615                 620
Gly Gly Gly Gly His His His His His His
625                 630
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<210> 11
<211> 1965
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
PL-deltaTaq

<220>
<221> CDS
<222> (1)..(1965)
<223> PL-deltaTaq

<400> 11
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aaaggcggcg gtgtcactag tggcgcaacc gtaaagttca agtacaaagg cgaagaaaaa 120
gaggtagaca tctccaagat caagaaagta tggcgtgtgg gcaagatgat ctccttcacc 180
tacgacgagg gcggtggcaa gaccggccgt ggtgcggtaa gcgaaaagga cgcgccgaag 240
gagctgctgc agatgctgga gaagcagaaa aagggcggcg gtgtcaccag tcccaaggcc 300
ctggaggagg ccccctggcc cccgccggaa ggggccttcg tgggctttgt gctttccgc 360
aaggagccca tgtgggccga tcttctggcc ctggccgccg ccaggggggg ccgggtccac 420
cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 480
aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgcccgg cgacgacccc 540
atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgagggggt ggcccggcgc 600
tacggcgggg agtggacgga ggaggcgggg gagcgggccg ccctttccga gaggctcttc 660
gccaacctgt gggggaggct tgaggggggag gagaggctcc tttggcttta ccgggaggtg 720
gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg 780
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag 840
gtcttccgcc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc 900
ctctttgacg agctagggct tcccgccatc ggcaagacgg agaagaccgg caagcgctcc 960
accagcgccg ccgtcctgga ggccctccgc gaggcccacc ccatcgtgga gaagatcctg 1020
cagtaccggg agctcaccaa gctgaagagc acctacattg acccccttgcc ggacctcatc 1080
caccccagga cgggccgcct ccacacccgc ttcaaccaga cggccacggc cacgggcagg 1140
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg 1200
atccgccggg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag 1260
atagagctca gggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag 1320
gaggggcggg acatccacac ggagaccgcc agctggatgt tcggcgtccc ccgggaggcc 1380
gtggaccccc tgatgcgccg ggcggccaag accatcaact tcggggtcct ctacggcatg 1440
tcggcccacc gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt 1500
gagcgctact ttcagagctt ccccaaggtg cgggcctgga ttgagaagac cctggaggag 1560
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagaccta 1620
gaggcccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc 1680
cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag 1740
gaaatggggg ccaggatgct ccttcaggtc cacgacgagc tggtcctcga ggccccaaaa 1800
gagagggcgg aggccgtggc ccggctggcc aaggaggtca tggaggggt gtatcccctg 1860
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc 1920
attgatggcc gcggcggagg cgggcatcat catcatcatc attaa 1965

<210> 12
<211> 654
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
PL-deltaTaq

<400> 12
Met Ile Thr Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg
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Lys Lys Lys Lys Lys Gly Gly Gly Val Thr Ser Gly Ala Thr Val Lys
20 25 30
Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
35 40 45
Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
50 55 60
Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
65 70 75 80

```
Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Gly Gly Gly Val Thr
                85                  90                  95
Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
            100                 105                 110
Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu
        115                 120                 125
Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu
    130                 135                 140
Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala
145                 150                 155                 160
Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro
                165                 170                 175
Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
            180                 185                 190
Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu
        195                 200                 205
Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp
    210                 215                 220
Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val
225                 230                 235                 240
Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val
                245                 250                 255
Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu
            260                 265                 270
Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro
        275                 280                 285
Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
    290                 295                 300
Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
305                 310                 315                 320
Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
                325                 330                 335
Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr
            340                 345                 350
Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His
        355                 360                 365
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
    370                 375                 380
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
385                 390                 395                 400
Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu
                405                 410                 415
Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
            420                 425                 430
Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu
        435                 440                 445
Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu
    450                 455                 460
Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
465                 470                 475                 480
Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
                485                 490                 495
Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
            500                 505                 510
Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
        515                 520                 525
Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val
    530                 535                 540
Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
545                 550                 555                 560
```

```
Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
                565                 570                 575
Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp
            580                 585                 590
Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg
        595                 600                 605
Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu
    610                 615                 620
Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly
625                 630                 635                 640
Ile Asp Gly Arg Gly Gly Gly Gly His His His His His His
                645                 650
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<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L71F

<400> 13
cctgctctgc cgcttcacgc 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L71R

<400> 14
gcacagcggc tggctgagga 20

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L18015F

<400> 15
tgacggagga taacgccagc ag 22

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L23474R

<400> 16
gaaagacgat gggtcgctaa tacgc 25

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L18015F

<400> 17
tgacggagga taacgccagc ag 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L29930R

<400> 18
ggggttggag gtcaatgggt tc 22

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L30350F

<400> 19
cctgctctgc cgcttcacgc 20

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L35121R

<400> 20
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<210> 21
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<210> 22
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<210> 23
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<210> 30
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tag

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1 5

<210> 31
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<210> 32
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<220>
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Gly Gly Val Thr
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<210> 33
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<220>
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<400> 33
Gly Thr Gly Gly Gly Gly
1 5

<210> 34
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<212> PRT
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<220>
<223> Description of Artificial Sequence:lysine-rich
peptide

<400> 34
Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg Lys Lys Lys
1 5 10 15
Gly Gly Gly Val Thr
20